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## RAW SEQUENCE LISTING

DATE: 01/23/2003

PATENT APPLICATION: US/10/058,518

TIME: 10:32:01

Input Set : A:\06501-097001.txt

Output Set: N:\CRF4\01232003\J058518.raw

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4 <110> APPLICANT: Ota, Toshio
5      Isogai, Takao
6      Nishikawa, Tetsuo
7      Hayashi, Koji
8      Otsuka, Kaoru
9      Yamamoto, Jun-ichi
10     Ishii, Shizuko
11     Sugiyama, Tomoyasu
12     Wakamatsu, Ai
13     Nagai, Keiichi
14     Otsuki, Tetsuji
15     Funahashi, Shin-ichi
16     Miyata, Shoji
18 <120> TITLE OF INVENTION: NOVEL GENES ASSOCIATED WITH THE
19     MAINTENANCE OF DIFFERENTIATION OF SMOOTH MUSCLE CELLS
21 <130> FILE REFERENCE: 06501-097001
23 <140> CURRENT APPLICATION NUMBER: US 10/058,518
24 <141> CURRENT FILING DATE: 2002-01-28
26 <150> PRIOR APPLICATION NUMBER: PCT/JP00/05059
27 <151> PRIOR FILING DATE: 2000-07-28
29 <150> PRIOR APPLICATION NUMBER: US 60/183,322
30 <151> PRIOR FILING DATE: 2000-02-17
32 <150> PRIOR APPLICATION NUMBER: US 60/159,590
33 <151> PRIOR FILING DATE: 1999-10-18
35 <150> PRIOR APPLICATION NUMBER: JP 11-248036
36 <151> PRIOR FILING DATE: 1999-07-29
38 <150> PRIOR APPLICATION NUMBER: JP 2000-118776
39 <151> PRIOR FILING DATE: 2000-01-11
41 <150> PRIOR APPLICATION NUMBER: JP 2000-183767
42 <151> PRIOR FILING DATE: 2000-05-02
44 <160> NUMBER OF SEQ ID NOS: 16
46 <170> SOFTWARE: FastSEQ for Windows Version 4.0
48 <210> SEQ ID NO: 1
49 <211> LENGTH: 2256
50 <212> TYPE: DNA
51 <213> ORGANISM: Homo sapiens
53 <220> FEATURE:
54 <221> NAME/KEY: CDS
55 <222> LOCATION: (125)...(1366)
57 <400> SEQUENCE: 1
58 cagtgcgcag gcgtgagcgg tcgggccccg acgcgcgcgg gtctcgtttg gagcggggagt      60
59 gagttcctga gcgagtgagc ccggcagcgg gcgatagggg ggccaggtgc ctccacagtc      120
60 agcc atg gca gcg ctg cgc tac gcg ggg ctg gac gac acg gac agt gag      169

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61	Met Ala Ala Leu Arg Tyr Ala Gly Leu Asp Asp Thr Asp Ser Glu	
62	1 5 10 15	
64	gac gag ctg cct ccg ggc tgg gag gag aga acc acc aag gac ggc tgg	217
65	Asp Glu Leu Pro Pro Gly Trp Glu Glu Arg Thr Thr Lys Asp Gly Trp	
66	20 25 30	
68	gtt tac tac gcc aat cac acc gag gag aag act cag tgg gaa cat cca	265
69	Val Tyr Tyr Ala Asn His Thr Glu Glu Lys Thr Gln Trp Glu His Pro	
70	35 40 45	
72	aaa act gga aaa aga aaa cga gtg gca gga gat ttg cca tac gga tgg	313
73	Lys Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp	
74	50 55 60	
76	gaa caa gaa act gat gag aac gga caa gtg ttt ttt gtt gac cat ata	361
77	Glu Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile	
78	65 70 75	
80	aat aaa aga acc acc tac ttg gac cca aga ctg gcg ttt act gtg gat	409
81	Asn Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp	
82	80 85 90 95	
84	gat aat ccg acc aag cca acc acc cgg caa aga tac gac ggc agc acc	457
85	Asp Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr	
86	100 105 110	
88	act gcc atg gaa att ctc cag ggc ccg gat ttc act ggc aaa gtg gtt	505
89	Thr Ala Met Glu Ile Leu Gln Gly Pro Asp Phe Thr Gly Lys Val Val	
90	115 120 125	
92	gtg gtc act gga gct aat tca gga ata ggg ttc gaa acc gcc aag tct	553
93	Val Val Thr Gly Ala Asn Ser Gly Ile Gly Phe Glu Thr Ala Lys Ser	
94	130 135 140	
96	ttt gcc ctc cat ggt gca cat gtg atc ttg gcc tgc agg aac atg gca	601
97	Phe Ala Leu His Gly Ala His Val Ile Leu Ala Cys Arg Asn Met Ala	
98	145 150 155	
100	agg gcg agt gaa gca gtg tca cgc att tta gaa gaa tgg cat aaa gcc	649
101	Arg Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Glu Trp His Lys Ala	
102	160 165 170 175	
104	aag gta gaa gca atg acc ctg gac ctc gct ctg ctc cgt agc gtg cag	697
105	Lys Val Glu Ala Met Thr Leu Asp Leu Ala Leu Leu Arg Ser Val Gln	
106	180 185 190	
108	cat ttt gct gaa gca ttc aag gcc aag aat gtg cct ctt cat gtg ctt	745
109	His Phe Ala Glu Ala Phe Lys Ala Lys Asn Val Pro Leu His Val Leu	
110	195 200 205	
112	gtg tgc aac gca gca act ttt gct cta ccc tgg agt ctc acc aaa gat	793
113	Val Cys Asn Ala Ala Thr Phe Ala Leu Pro Trp Ser Leu Thr Lys Asp	
114	210 215 220	
116	ggc ctg gag acc acc ttt caa gtg aat cat ctg ggg cac ttc tac ctt	841
117	Gly Leu Glu Thr Thr Phe Gln Val Asn His Leu Gly His Phe Tyr Leu	
118	225 230 235	
120	gtc cag ctc ctc cag gat gtt ttg tgc cgc tca gct cct gcc cgt gtc	889
121	Val Gln Leu Leu Gln Asp Val Leu Cys Arg Ser Ala Pro Ala Arg Val	
122	240 245 250 255	
124	att gtg gtc tcc tca gag tcc cat cga ttt aca gat att aac gac tcc	937
125	Ile Val Val Ser Ser Glu Ser His Arg Phe Thr Asp Ile Asn Asp Ser	

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126          260          265          270
128 ttg gga aaa ctg gac ttc agt cgc ctc tct cca aca aaa aac gac tat      985
129 Leu Gly Lys Leu Asp Phe Ser Arg Leu Ser Pro Thr Lys Asn Asp Tyr
130          275          280          285
132 tgg gcg atg ctg gct tat aac agg tcc aag ctc tgc aac atc ctc ttc      1033
133 Trp Ala Met Leu Ala Tyr Asn Arg Ser Lys Leu Cys Asn Ile Leu Phe
134          290          295          300
136 tcc aac gag ctg cac cgt cgc ctc tcc cca cgc ggg gtc acg tcg aac      1081
137 Ser Asn Glu Leu His Arg Arg Leu Ser Pro Arg Gly Val Thr Ser Asn
138          305          310          315
140 gca gtg cat cct gga aat atg atg tac tcc aac att cat cgc agc tgg      1129
141 Ala Val His Pro Gly Asn Met Met Tyr Ser Asn Ile His Arg Ser Trp
142          320          325          330
144 tgg gtg tac aca ctg ctg ttt acc ttg gcg agg cct ttc acc aag tcc      1177
145 Trp Val Tyr Thr Leu Leu Phe Thr Leu Ala Arg Pro Phe Thr Lys Ser
146          340          345          350
148 atg caa cag gga gct gcc acc acc gtg tac tgt gct gct gtc cca gaa      1225
149 Met Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu
150          355          360          365
152 ctg gag ggt ctg gga ggg atg tac ttc aac aac tgc tgc cgc tgc atg      1273
153 Leu Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met
154          370          375          380
156 ccc tca cca gaa gct cag agc gaa gag acg gcc cgg acc ctg tgg gcg      1321
157 Pro Ser Pro Glu Ala Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala
158          385          390          395
160 ctc agc gag agg ctg atc caa gaa cgg ctt ggc agc cag tcc ggc      1366
161 Leu Ser Glu Arg Leu Ile Gln Glu Arg Leu Gly Ser Gln Ser Gly
162          400          405          410
164 taagtggagc tcagagcgga tgggcacaca caccgcctt gtgtgtgtcc cctcacgcaa      1426
165 gtgccagggc tgggcccctt ccaaatgtcc ctccaacaca gatccgcaag agtaaaggaa      1486
166 ataagagcag tcacaacaga gtgaaaaatc ttaagtacca atgggaagca gggaattcct      1546
167 ggggtaaaagt atcacttttc tggggctggg ctaggcatag gtctctttgc tttctggtgg      1606
168 tggcctgttt gaaagtaaaa acctgcttgg tgtgtagggt ccgatatctc ctggagaagc      1666
169 accagcaatt ctctttcttt tactgttata gaatagcctg aggtcccctc gtcccatcca      1726
170 gctaccacca cggccaccac tgcagccggg ggctggcctt ctctactta gggaagaaaa      1786
171 agcaagtgtt cactgctcct tgctgcattg atccaggaga taattgtttc attcatcctg      1846
172 accaagactg agccagctta gcaactgctg gggagacaaa tctcagaacc ttgtcccagc      1906
173 cagtgaggat gacagtgaac cccagaggga gtagaatacg cagaactacc aggtggcaaa      1966
174 gtacttgtca tagactcctt tgctaattgct atgcaaaaaa ttcttttagag attataacaa      2026
175 atttttcaaaa tcatctcctta gataccttga aaggcaggaa gggaagcgta tataacttaag      2086
176 aatacacagg atattttggg gggcagagaa taaaacgtta gttaatccct ttgtctgtca      2146
177 atcacagtct cagttctctt gctttcacat tgtacttaaa cctcctgctg tgccctcgcat      2206
178 cctatgctta ataaaaaagac atgcttgaat atcaaaaaaa aaaaaaaaaaac      2256
180 <210> SEQ ID NO: 2
181 <211> LENGTH: 414
182 <212> TYPE: PRT
183 <213> ORGANISM: Homo sapiens
185 <400> SEQUENCE: 2
186 Met Ala Ala Leu Arg Tyr Ala Gly Leu Asp Asp Thr Asp Ser Glu Asp

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```

187 1 5 10 15
188 Glu Leu Pro Pro Gly Trp Glu Glu Arg Thr Thr Lys Asp Gly Trp Val
189 20 25 30
190 Tyr Tyr Ala Asn His Thr Glu Glu Lys Thr Gln Trp Glu His Pro Lys
191 35 40 45
192 Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp Glu
193 50 55 60
194 Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile Asn
195 65 70 75 80
196 Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp Asp
197 85 90 95
198 Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr Thr
199 100 105 110
200 Ala Met Glu Ile Leu Gln Gly Pro Asp Phe Thr Gly Lys Val Val Val
201 115 120 125
202 Val Thr Gly Ala Asn Ser Gly Ile Gly Phe Glu Thr Ala Lys Ser Phe
203 130 135 140
204 Ala Leu His Gly Ala His Val Ile Leu Ala Cys Arg Asn Met Ala Arg
205 145 150 155 160
206 Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Glu Trp His Lys Ala Lys
207 165 170 175
208 Val Glu Ala Met Thr Leu Asp Leu Ala Leu Leu Arg Ser Val Gln His
209 180 185 190
210 Phe Ala Glu Ala Phe Lys Ala Lys Asn Val Pro Leu His Val Leu Val
211 195 200 205
212 Cys Asn Ala Ala Thr Phe Ala Leu Pro Trp Ser Leu Thr Lys Asp Gly
213 210 215 220
214 Leu Glu Thr Thr Phe Gln Val Asn His Leu Gly His Phe Tyr Leu Val
215 225 230 235 240
216 Gln Leu Leu Gln Asp Val Leu Cys Arg Ser Ala Pro Ala Arg Val Ile
217 245 250 255
218 Val Val Ser Ser Glu Ser His Arg Phe Thr Asp Ile Asn Asp Ser Leu
219 260 265 270
220 Gly Lys Leu Asp Phe Ser Arg Leu Ser Pro Thr Lys Asn Asp Tyr Trp
221 275 280 285
222 Ala Met Leu Ala Tyr Asn Arg Ser Lys Leu Cys Asn Ile Leu Phe Ser
223 290 295 300
224 Asn Glu Leu His Arg Arg Leu Ser Pro Arg Gly Val Thr Ser Asn Ala
225 305 310 315 320
226 Val His Pro Gly Asn Met Met Tyr Ser Asn Ile His Arg Ser Trp Trp
227 325 330 335
228 Val Tyr Thr Leu Leu Phe Thr Leu Ala Arg Pro Phe Thr Lys Ser Met
229 340 345 350
230 Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu Leu
231 355 360 365
232 Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met Pro
233 370 375 380
234 Ser Pro Glu Ala Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala Leu
235 385 390 395 400

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236 Ser Glu Arg Leu Ile Gln Glu Arg Leu Gly Ser Gln Ser Gly
237           405           410
239 <210> SEQ ID NO: 3
240 <211> LENGTH: 251
241 <212> TYPE: DNA
242 <213> ORGANISM: Gallus gallus
244 <220> FEATURE:
245 <221> NAME/KEY: CDS
246 <222> LOCATION: (3)...(251)
248 <400> SEQUENCE: 3
249 ag gag cgc acc acc aag gac ggc tgg gtt tac tac gcc aat cac ttg      47
250   Glu Arg Thr Thr Lys Asp Gly Trp Val Tyr Tyr Ala Asn His Leu
251     1           5           10           15
253 gaa gaa aaa aca cag tgg gaa cat cca aaa tct ggg aag agg aaa cgt      95
254 Glu Glu Lys Thr Gln Trp Glu His Pro Lys Ser Gly Lys Arg Lys Arg
255           20           25           30
257 gtt gca gga ggt ctg cca tat gga tgg gag cag gag act gat gaa aat      143
258 Val Ala Gly Gly Leu Pro Tyr Gly Trp Glu Gln Glu Thr Asp Glu Asn
259           35           40           45
261 gga cag gtc tat ttt gta gac cac ata aac aaa aga act acc tat ctg      191
262 Gly Gln Val Tyr Phe Val Asp His Ile Asn Lys Arg Thr Thr Tyr Leu
263           50           55           60
265 gat cca aga ttg gcc ttt aca gtt gaa gat aat cca gca aag cca cct      239
266 Asp Pro Arg Leu Ala Phe Thr Val Glu Asp Asn Pro Ala Lys Pro Pro
267     65           70           75
269 act aga caa aaa      251
270 Thr Arg Gln Lys
271 80
274 <210> SEQ ID NO: 4
275 <211> LENGTH: 83
276 <212> TYPE: PRT
277 <213> ORGANISM: Gallus gallus
279 <400> SEQUENCE: 4
280 Glu Arg Thr Thr Lys Asp Gly Trp Val Tyr Tyr Ala Asn His Leu Glu
281 1           5           10           15
282 Glu Lys Thr Gln Trp Glu His Pro Lys Ser Gly Lys Arg Lys Arg Val
283           20           25           30
284 Ala Gly Gly Leu Pro Tyr Gly Trp Glu Gln Glu Thr Asp Glu Asn Gly
285           35           40           45
286 Gln Val Tyr Phe Val Asp His Ile Asn Lys Arg Thr Thr Tyr Leu Asp
287     50           55           60
288 Pro Arg Leu Ala Phe Thr Val Glu Asp Asn Pro Ala Lys Pro Pro Thr
289 65           70           75           80
290 Arg Gln Lys
292 <210> SEQ ID NO: 5
293 <211> LENGTH: 30
294 <212> TYPE: RNA
295 <213> ORGANISM: Artificial Sequence
297 <220> FEATURE:

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/058,518

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Input Set : A:\06501-097001.txt

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